

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/807, 647

Source: PCT 09

Date Processed by STIC: 5-1-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

New Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>09/807, 647</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input checked="" type="checkbox"/> Use of "Artificial" (NEW RULES)	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. <u>Valid response is Artificial Sequence.</u>	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/807,647

DATE: 05/01/2001
TIME: 11:36:29

Input Set : A:\2560US0P.sequence.list.txt
Output Set: N:\CRF3\05012001\I807647.raw

Does Not Comply
Corrected Diskette Needed
global error

3 <110> APPLICANT: OI, Satoru
4 SUZUKI, Nobuhiro
5 MATSUMOTO, Takahiro
7 <120> TITLE OF INVENTION: 1,5-Benzodiazepine Compounds, Their Production and Use
9 <130> FILE REFERENCE: 2560US0P
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/807,647
C--> 11 <141> CURRENT FILING DATE: 2001-04-16
11 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05754
12 <151> PRIOR FILING DATE: 1999-10-19
14 <150> PRIOR APPLICATION NUMBER: JP 10-298941
15 <151> PRIOR FILING DATE: 1998-10-20
19 <160> NUMBER OF SEQ ID NOS: 10
W--> 20 <210> SEQ ID NO: 1
21 <211> LENGTH: 30
22 <212> TYPE: DNA
C--> 23 <213> ORGANISM: Artificial
W--> 24 <220> FEATURE:
25 <223> OTHER INFORMATION: primer
W--> 26 <400> SEQUENCE: 1
27 ggtcgacctc agcttaggatg ttcccaatg 30
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 28
31 <212> TYPE: DNA
C--> 32 <213> ORGANISM: Artificial
W--> 33 <220> FEATURE:
34 <223> OTHER INFORMATION: primer
W--> 35 <400> SEQUENCE: 2
36 ggtcgacccg ggctcagagc gtcgtatg 28
38 <210> SEQ ID NO: 3
39 <211> LENGTH: 28
40 <212> TYPE: DNA
C--> 41 <213> ORGANISM: Artificial
W--> 42 <220> FEATURE:
43 <223> OTHER INFORMATION: primer
W--> 44 <400> SEQUENCE: 3
45 ggtcgacacc atggacatgg cggatgag 28
47 <210> SEQ ID NO: 4
48 <211> LENGTH: 26
49 <212> TYPE: DNA
C--> 50 <213> ORGANISM: Artificial
W--> 51 <220> FEATURE:
52 <223> OTHER INFORMATION: primer
W--> 53 <400> SEQUENCE: 4
54 ggtcgacagt tcagatactg gtttgg 26
56 <210> SEQ ID NO: 5
57 <211> LENGTH: 30
58 <212> TYPE: DNA

Incomplete response
for <213> as per section
1.823 b of new sequence
rules. See # 11 on the
Error Summary Sheet.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,647

DATE: 05/01/2001

TIME: 11:36:29

Input Set : A:\2560US0P.sequence.list.txt
Output Set: N:\CRF3\05012001\I807647.raw

C--> 59 <213> ORGANISM: Artificial
W--> 60 <220> FEATURE:
61 <223> OTHER INFORMATION: primer
W--> 62 <400> SEQUENCE: 5
63 ggtcgacctc aaccatggac atgcttcatc 30
65 <210> SEQ ID NO: 6
66 <211> LENGTH: 29
67 <212> TYPE: DNA
C--> 68 <213> ORGANISM: Artificial
W--> 69 <220> FEATURE:
70 <223> OTHER INFORMATION: primer
W--> 71 <400> SEQUENCE: 6
72 ggtcgacttt ccccgaggccc ctacaggtt 29
74 <210> SEQ ID NO: 7
75 <211> LENGTH: 28
76 <212> TYPE: DNA
C--> 77 <213> ORGANISM: Artificial
W--> 78 <220> FEATURE:
79 <223> OTHER INFORMATION: primer
W--> 80 <400> SEQUENCE: 7
81 ggctcgagtc accatgagcg cccctcg 28
83 <210> SEQ ID NO: 8
84 <211> LENGTH: 27
85 <212> TYPE: DNA
C--> 86 <213> ORGANISM: Artificial
W--> 87 <220> FEATURE:
88 <223> OTHER INFORMATION: primer
W--> 89 <400> SEQUENCE: 8
90 gggctcgagc tcctcagaag gtgggtgg 27
92 <210> SEQ ID NO: 9
93 <211> LENGTH: 28
94 <212> TYPE: DNA
C--> 95 <213> ORGANISM: Artificial
W--> 96 <220> FEATURE:
97 <223> OTHER INFORMATION: primer
W--> 98 <400> SEQUENCE: 9
99 ggtcgaccac catggagccc ctgttccc 28
101 <210> SEQ ID NO: 10
102 <211> LENGTH: 26
103 <212> TYPE: DNA
C--> 104 <213> ORGANISM: Artificial
W--> 105 <220> FEATURE:
106 <223> OTHER INFORMATION: primer
W--> 107 <400> SEQUENCE: 10
108 ccgtcgacac tctcacagct tgctgg 26

See p. 1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/807,647

DATE: 05/01/2001

TIME: 11:36:30

Input Set : A:\2560US0P.sequenceclist.txt

Output Set: N:\CRF3\05012001\I807647.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:283 W: Missing Blank Line separator, <210> field identifier
L:23 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:24 M:283 W: Missing Blank Line separator, <220> field identifier
L:26 M:283 W: Missing Blank Line separator, <400> field identifier
L:32 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:33 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:283 W: Missing Blank Line separator, <400> field identifier
L:41 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:42 M:283 W: Missing Blank Line separator, <220> field identifier
L:44 M:283 W: Missing Blank Line separator, <400> field identifier
L:50 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:51 M:283 W: Missing Blank Line separator, <220> field identifier
L:53 M:283 W: Missing Blank Line separator, <400> field identifier
L:59 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:60 M:283 W: Missing Blank Line separator, <220> field identifier
L:62 M:283 W: Missing Blank Line separator, <400> field identifier
L:68 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:69 M:283 W: Missing Blank Line separator, <220> field identifier
L:71 M:283 W: Missing Blank Line separator, <400> field identifier
L:77 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:78 M:283 W: Missing Blank Line separator, <220> field identifier
L:80 M:283 W: Missing Blank Line separator, <400> field identifier
L:86 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:87 M:283 W: Missing Blank Line separator, <220> field identifier
L:89 M:283 W: Missing Blank Line separator, <400> field identifier
L:95 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:96 M:283 W: Missing Blank Line separator, <220> field identifier
L:98 M:283 W: Missing Blank Line separator, <400> field identifier
L:104 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:105 M:283 W: Missing Blank Line separator, <220> field identifier
L:107 M:283 W: Missing Blank Line separator, <400> field identifier